

## APPENDIX

### BestFit Results

BESTFIT of: 1587\_SEQ\_1 check: 9861 from: 1 to: 590

to: 7071378\_SEQ\_1 check: 9103 from: 1 to: 531

WPDEF ESR1 PRO - disclosed, not patented; ESR 1 of Figure 4

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	162	Length:	39
Ratio:	4.154	Gaps:	0
Percent Similarity:	69.231	Percent Identity:	69.231

Match display thresholds for the alignment(s):

| = IDENTITY

: = 5

. = 1

1587\_SEQ\_1 x 7071378\_SEQ\_1 December 15, 2006 16:23 ..

```
      .      .      .
199 tttactaaaatttttctctgtatagtaacatgtcataact 237
    |||| |||| | ||| |||| || ||||| |
355 tttattaaaactgtctttaaataaggccaagtcataaat 393
```

Input Sequence: 1587\_SEQ\_1

!!NA\_SEQUENCE 1.0

1587\_SEQ\_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```
1  gaattcgccc ttggtagatg tctagatgac ctattctact tttcctaaga
51  ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaa aaaacgccag tcatatatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagtttc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatatatggt acgggattaa taggttccaa aaaccagccg
301 taacctattd atattagggt actttaagct ggtgccctca gttttgttgg
```

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```
351  tgtcttcggtt tttaaactta gttgtatattt ttttcttagt tctgtccttc
401  tagtggttata gagcataagg acaaaattga gcaaaaaatg actaaggata
451  aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501  ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551  tggatttgca ttgtcagtca ggccagtcaa ggggaccatg
```

Input Sequence: 7071378\_SEQ\_1

!!NA\_SEQUENCE 1.0

WPDEF ESR1 PRO - disclosed, not patented; ESR 1 of Figure 4

7071378\_SEQ\_1 Length: 531 December 15, 2006 16:20 Type: N Check: 9103

..

```
1  gatcattaag gactaagcag tctttttccc tttcggcttg catcatcttt
51  agtcttcata actattataa gccgaagcta ttacccttg gctatagctt
101  cgggtgttcac ctttattata ttcggactat gtcttcacct tgtataacct
151  tgtcttgggg gaaaaccttc atcctgaagc cgaagctccc tgtaataatt
201  catatcatgc taaaaataaa tggtcagtcc tgtttttgag gaccttcgga
251  agaggaaggc cccccaacaa gacgattaac tagtattgtc tcaactgcatt
301  gtttttttgg cacttcatca ataatgcctc aatagcatac ttcatttttag
351  gaactttatt aaaactgtct taaaataggg ccaagtcata aattcattca
401  aagtgactct tcatttctta cttcctatct ttggtgggtt tgtatatata
451  tatgttcacg gttgagtgat gttcctacac cactacacca cacgttagat
501  atatatacag aaaatagctt cactatctag a
```

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BestFit Results

BESTFIT of: 1587\_SEQ\_1 check: 9861 from: 1 to: 590

to: 7071378\_SEQ\_2 check: 806 from: 1 to: 2493

WPDEF Bonello patented promoter; ESR 2 of Fig. 4 begins at position 1986

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	139	Length:	31
Ratio:	4.484	Gaps:	0
Percent Similarity:	70.968	Percent Identity:	70.968

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 5  
. = 1

1587\_SEQ\_1 x 7071378\_SEQ\_2 December 15, 2006 15:59 ..

```
      .           .           .  
526 agtataactccaagcacatttgaatttggatt 556  
    | | | | | | | | | | | | | | | |  
525 atttttagacaaaaccatttaaatttggttt 555
```

Input Sequence: 1587\_SEQ\_1

!!NA\_SEQUENCE 1.0

1587\_SEQ\_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```
1  gaattcgccc ttggtagatg tctagatgac ctattctact tttcctaaga  
51  ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg  
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca  
151 agaaccagcc acaatccatt tattagtttc atataaatgt cataaatttt  
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa  
251 aaacgccagt tatttatggg acgggattaa taggttccaa aaaccagccg  
301 taacctatth atattagggt actttaagct ggtgccctca gttttgttgg  
351 tgtcttcggt tttaaactta gttgtattht ttttcttagt tctgtccttc
```

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```
401 tagtggttata gagcataagg acaaaattga gcaaaaaatg actaaggata
451 aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcaa ggggaccatg
```

Input Sequence: 7071378\_SEQ\_2

!!NA\_SEQUENCE 1.0  
WPDEF Bonello patented promoter; ESR 2 of Fig. 4 begins at position 1986  
7071378\_SEQ\_2 Length: 2493 December 15, 2006 15:57 Type: N Check: 806  
..

```
1 aagcttttcc ggtgatgaag cacctgtaat acttaacagc atgctgaaaa
51 caaatagtta gctgtgtttt tgaggacctt cggaagatga agggcccccac
101 cacatcccat gcatcaagtc cccatgactt gcaaaaaagc aaatttttatc
151 aaaattttctc ataaaacact tgaaaacatt tctcttttttg aaaagtgtag
201 agcactagca actgtctact aaaaagggttc ccaaattttct ggggtataaca
251 atcgcatggg aaataacaca aaggaaatcc tactaagagc agtaatttgg
301 ctaaaacaat agtgagcatt ttaatgtaat agggaatagg agcatgcaat
351 acttgtgttc tttcaggggtt ttgatgtcct caaaagtgtg cccccctggg
401 gcagttgcaa cactcaaaat ctactcgtat acataaagaa acatggggcac
451 aaaataagaa acaataactca aattatgaaa aagggttcaaa tgggtcctata
501 attattgtag acatttttaga atttatttta gaccaaaacc atttaaattt
551 ggttttaaat gagttagata ttaatattta ttcagtttat agttatttgg
601 gacatttatt tacttaacta taacttctag ggttttataaa gtaaattttg
651 ggtccctagt tggaactagc tcagattgct ggttgatttc cataaaagtc
701 gaggttcctt tagcaaaaat ccacggtgaa caagggggag ataggtgttg
751 accgatatct ctaaattttg atcgttggac ggcacatgga tgtctcagat
```

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801 taaatggtgg atgtgcaagc gacgcgcaca cgatggagga atggcttcac  
851 gacggtgggc tactagagct ggctacgtca accaatggag ggctcgggtca  
901 aggtcaaaat ttgttgccaa gccactgtgg ctcacgatga gtcgattgag  
951 cacatatcaa ggtcgagggt caaccagagg ggcaagatcg atggtgcagt  
1001 ggtgttctcg atggaagggg aaacttcggt gagcaattca agatttccta  
1051 tcatgtgacc gggtcaggga atgggcgcacat ggggtttgggt accttctggt  
1101 gcacatcatg ttgctgtatc gatgtcaagg gagcattagg gttcacgagt  
1151 cagcgatgac gggcatggtg ggacttgtgt caccatgggt cgatcaacta  
1201 gggacgatag agctctatga agtttcacaa cttcctcaca ctctagggat  
1251 catggtgaca aagggtgggga ggacggggcg tctctagtga ggggtggaatg  
1301 cagttctgtc acgtgggaat agtggcgcca tcgcttgtaa tgaataaaag  
1351 gtgcttgggt ggctgggaag tgcaatatga ggggaagtagt tgggtgcgggg  
1401 atgttccttt tataaggag caccattgat taatggaaga caatgacaca  
1451 aagggtggtg cgacagtta aagctcgaat gctgctaggg gtgctcaagg  
1501 ttaaaagatc aggcacagg gaggaaggc agggataaaa tttctttact  
1551 ccagttgtgg ggtgatggg acaagggtag tgctcaagca agggagggcg  
1601 agttcagcgc agagatgcct gttgtgacac atgggggggg ggggaattgga  
1651 ggttgggggt gaccaggtga cgttatggcg tgaccagag aagagacca  
1701 ctgatgggga aaaaagggtgc caacagggtg ggaccaagg gtcagtgact  
1751 caccgtgaca tgttattgga aagttacgtc cggaatgggt tgggcctgag  
1801 tgatctaggc tggctcgggc actgtgctga tcctttaatt tctccattcc  
1851 caatttaagt tgaattttta attcaaatca aatgactcca aatctctcca  
1901 aaattaccaa aatatagaat atttagatga atatgttgggt ggagtttggg  
1951 ctccgctttt ggttagtatg tttgtataaa aataatttct ctccctttgt  
2001 cacttccaat attgacttaa atttttatgt agcaatgcc aactttttta  
2051 gtagtgtgcc acttatagca caaaaactat atccattttc taatagtcct  
2101 tgaaatccac attctatttt tagccattct tcaaaattgg cacaaaacta

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2151 ggaaaattta atacattctt gccataacat attctagtgc aaatgttaac  
2201 tagattgctc aatattagca aacttctttt gtaagattca ttaatattgc  
2251 tacattgcat acttttttag aagttcatca ataatgcctc attagcatac  
2301 ttcatttttag gaacttgatt aaaaccgcct taaaatagag ccaagtgacg  
2351 gatccattta aaggatgatt ttaatttctt acttcctatc tttggtggct  
2401 tatgtttata tatgtgtggg tggttgaatg atgttcctac accactacac  
2451 cacacgttgg acatatatat ggaaaatagc ttcacagtct aga

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BestFit Results

BESTFIT of: 1587\_SEQ\_1 check: 9861 from: 1 to: 590

to: 7071378\_SEQ\_3 check: 9984 from: 1 to: 1708

WPDEF ESR 3 PRO - disclosed, not patented; ESR3 of Fig. 4 begins at position 1193

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	165	Length:	45
Ratio:	3.667	Gaps:	0
Percent Similarity:	66.667	Percent Identity:	66.667

Match display thresholds for the alignment(s):

| = IDENTITY

: = 5

. = 1

1587\_SEQ\_1 x 7071378\_SEQ\_3 December 15, 2006 16:24 ..

```
      .      .      .      .
199 tttactaaaattttctctgtatagtaacatgtcataactgaactt 243
    |||| ||||| ||| |||| || |||| || | ||||
1529 tttatgaaaattgtcttaaaatagggccaagtcacaaatccactt 1573
```

Input Sequence: 1587\_SEQ\_1

!!NA\_SEQUENCE 1.0

1587\_SEQ\_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```
1  gaattcgccc ttggtagatg tctagatgac ctattctact tttcctaaga
51  ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagtttc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatttatggt acgggattaa taggttccaa aaaccagccg
301 taacctattt atattagggt actttaagct ggtgccctca gttttgttgg
351 tgtcttcggt tttaaactta gttgtatttt ttttcttagt tctgtccttc
```

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```
401  tagtgttata gagcataagg acaaaattga gcaaaaaatg actaaggata
451  aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501  ttcaaaagga caccagtcta taaaagtat actccaagca catttgaatt
551  tggatttgca ttgtcagtca ggccagtcaa ggggaccatg
```

Input Sequence: 7071378\_SEQ\_3

!!NA\_SEQUENCE 1.0

WPDEF ESR 3 PRO - disclosed, not patented; ESR3 of Fig. 4 begins at  
position 1193

7071378\_SEQ\_3 Length: 1708 December 15, 2006 16:22 Type: N Check: 9984

..

```
1   aagcttagaa attttaaaaa aagccaggca agcgttggtg tgcaaagagc
51  taaaaattag gaagacaaga gaacacggca agaaagcatg ctaaattgtc
101 tcgcggtgcg ttcttattta tacgctcaat acgttgcaag tggtagggcc
151 ccacttgta ttgactattg ctattctagc aaagggaagg tgtttttcgg
201 accttcggct taaggccttc gtccatatcg caatctgaat ttatcattct
251 aacaaattaa tattgtgagg ggctactggt gggggccttc gacttcggaa
301 ggtcctcaaa aactggttta acagtgtttc tggagtataa tgcataaaca
351 ggtatcttcg ggtttggatc agaactaca catgaagagg cacaaagaac
401 acgaagggtg ggcagagcc gaagctcacg tgtaggagag cttcggcacg
451 acagcagaaa aagggaaccg acttaaaagg aaaggctatt cagacctcga
501 tggatttcta taggtcatta gcaaatgtaa agggcatgaa tgtaatttta
551 catgggctgt gtccttgcc ataaatagat gaacagtact ctcgactgtt
601 tcacgtgac ttggcattcg ctttttgcat cacgcttgta cccttgcttt
651 ccttcaaacc gaaggtaacat ctataatttg ttattgtggt attgtggata
701 tggtaatgca aataaaaata agttgatgat aatgtttata ttatttttcg
```



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751 tattttcatat atgaattctt cctcatcatt tattgtgctt acgaaggttt  
801 ttccttcaaa atctttgtcc ggaattcatt atatccgaag ggaaataatg  
851 tctcgaagga cgaaggactt tgatatttaa cacttttcat gttgccttgt  
901 tcttgactct tagcatttga gaacaagtcc ccaacagctc ctaagctctt  
951 ctttgaagaa acaactacta gatgaagttt ctccaaaagt acgtccattg  
1001 aatggagtaa agagtcattt gacctctcgg aataaaatta aaatgagaat  
1051 aagtaagaat aaaacacctc tattatcaaa tctaggccat acaaacattg  
1101 ggtattacta aaaaatagct aatgccatct ttcaacattt ggaagttaaa  
1151 accaaccaat cctcactcat tcccaagaaa tattggatca tatttaacat  
1201 tttgtgtcac ttacaaaaat ggcttaatct tttatgcggc aatgccaacc  
1251 ttttttagca ggggtgccact tgtaacatga aaactataac tattttcaaa  
1301 tagtaccttg aaattcgcat tctattttta tgcattcttc aaaattgaca  
1351 caaattaaac taggagaatt caatacatto ttgccataac atattcta  
1401 gcaaatatta agtagattgc tcaacatcgg tacacatctt ttggacgatt  
1451 aattagtatt gtctcactac attctttgtt ttagcagttc atcaataatg  
1501 cctcaatagc atacttcatt ttaggaactt tatgaaaatt gtcttaaaat  
1551 agggccaagt cacaaatcca cttcaaagggt gactcttcat ttcttacttc  
1601 ctatctttgc ttgtttttgt atatatatgt gtggatgggt gagtgatggt  
1651 cctacaccac tacaccacac cttagacaca tatatggaaa atagcttcac  
1701 tgtctaga

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#### BestFit Results

BESTFIT of: 1587\_SEQ\_1 check: 9861 from: 1 to: 590

to: 6777591\_SEQ\_1 check: 2029 from: 1 to: 4305

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	169	Length:	67
Ratio:	2.770	Gaps:	2
Percent Similarity:	72.131	Percent Identity:	72.131

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 5  
. = 1

1587\_SEQ\_1 x 6777591\_SEQ\_1 December 15, 2006 17:07 ..

```
161 acaatccatttattagtttcatataaatgtcata....aattttta..ct 204
    ||||| || | || | ||| ||| ||| |||| ||| ||
956 acaatcaatatgataataataataataataattcaattattaatct 1005
    .
205 aaaattttctctgtata 221
    | ||||| | |||
1006 acaattttttaattata 1022
```

Input Sequence: 1587\_SEQ\_1

!!NA\_SEQUENCE 1.0

1587\_SEQ\_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```
1 gaattcgccc ttggtagatg tctagatgac ctattctact tttcctaaga
51 ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagtttc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatttatggg acgggattaa taggttccaa aaaccagccg
301 taacctatth atattagggt actttaagct ggtgccctca gttttgttgg
```

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```
351  tgtcttcggtt tttaaactta gttgtatattt ttttcttagt tctgtccttc
401  tagtggttata gagcataagg acaaaattga gcaaaaaatg actaaggata
451  aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501  ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551  tggatttgca ttgtcagtca ggccagtcaa ggggaccatg
```

Input Sequence: 6777591\_SEQ\_1

!!NA\_SEQUENCE 1.0  
6777591\_SEQ\_1 Length: 4305 December 15, 2006 17:05 Type: N Check: 2029  
..

```
1  ttcaaaaccc gattcccgag gcggccctat tgaagatatg ggggaagtgc
51  gacgagatcg atgtcgggtc gagtgtctatg gtgatggtgc cgtttggggg
101  gaggatgagc gagatagcca agactagcat tccgttccca cacagagtgc
151  ggaatttgta ccaaattcaa cacttgctgt attggagcga cgatagggac
201  gcggaaaaac acatccgttg gatcagggag ttgtacgatg atctcgagcc
251  ttatgtgtcg aagaatccga ggtatgctta cgtgaactac agggatctcg
301  acatcgggat gaatggagga ggtgaagggg atgagaaggg tacttatggt
351  gaggctaagg tgtgggggga gaagtacttt ggggtcaact ttgatcggtt
401  ggttcgggtg aagacgattg ttgatcccaa taatgtgttt cgaaacgagc
451  agagcattcc ctcaattcca actcggttat aaggatcaat gatcaatgag
501  aattttcctt tccaatgtga ttacaagtgc tattgggtca gctttctcaa
551  ctgctcctat tcatttagat taattcataa caactattaa tttaccagcc
601  ttttatccgg ccggttgggc gatttatattt cttaagtttt agatgaaatg
651  aaaccgattt agtttttatt gagatgagat taatcttaat ttgcttgaaa
701  tttactcacg gttgatgtga tatttggaat taactaaaat gataaatatc
```

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751 ggataaaaaat aaaaatatattt aaaataaata acataaacat aagaacaata  
801 aaataaataa atttaattttt aattttatttc cttgttttct ttctgtatca  
851 tacatctctt ctcttacttc ttaaaggctt ttcaattatc acttaattaa  
901 atacaataga taaatcggtta attctataac attaacctat acacttgcac  
951 ggtgaacaat caatatgata atataataat aatataataa ttcaattatt  
1001 aatctacaat tttttaatta taaagtttat gcggtcagtt tctgcaagct  
1051 ccgagctcct tgtcatcggt agtttctgcg gtctcaaggt ataacgactc  
1101 ggagcgacga gccctttgct tccaatggac gggttgcatt tctgccgtcg  
1151 ttgagctcga ttggcgtgtc atgctggagt cagagttcct acaaaaaaac  
1201 cctaaactag agggtgatta gggtgaaatt aggggtgttg cctggggtcc  
1251 attgtccaaa gttttagtca acttaaaaaac agacttaaat tttatgcttc  
1301 aaaatagttt atctgttatt atattagcgt gtaattagtc ttgacaatgg  
1351 ggccggacgg gtacggattc gggacccga tccccgcca tagtgtaatg  
1401 gctcaactgc caagtcagca ttggaccgaa attattggac acgaagtact  
1451 aatgtgaaaa actttacatt tgttattttc tactttaata ctatgctatt  
1501 ttcaaaattt gaactttaat actatgtttt tatatagttt agtatatctt  
1551 aatttttatg caaattcatc taattgtatt aaactatttt cgatccgtag  
1601 ctaattattt cgaaggcaag tcaaagtgtt attgtggact atgtgagcta  
1651 atattgaacc tttatctctc ccaaccactc aagttaattg aaccaaactc  
1701 gatcggttg gtttcgagct atttcgagcc attgttggtta tatgcacgtg  
1751 agatatcaag attgaccgga acactttatt atgataatgt agaaaaagaa  
1801 aacatattct aagactacat gcatgcaaag tgcaaccct gcatggaaag  
1851 ctgctcaaca cgtggcatag actcccgcca cgtgtccatt ccacctcatc  
1901 acctcacccc caccgttcac ctcttattat atcacaacaa tcaatcaatc  
1951 ctactcctcc atactcgaac aaatccgacc aacttatacc aatattccca  
2001 aacttgatta atttctcagc aatatggatc agacgcacca gacatacgcc  
2051 ggaaccacgc agaaccgag ctatggcggc gggggcaciaa tgtaccagca

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2101 gcagcagccg aggtcttacc aggcgggtgaa ggcgggccact gcagccaccg  
2151 cgggtggatc cctcatcggt ctgtccggtc tcatccttac ggccaccgtc  
2201 atttcactca tcatagccac ccctctcctt gtcattcttca gccctgttct  
2251 tgtcccggtc ctcatcaccg tcgggctctt gatcaccggg tttcttgctt  
2301 ccggtgggtt cggagtcgcc gccgtcaccg tcttgtcctg gatctatagg  
2351 tatgtataag ctttggactt tagtattgtt ataaaataca taagctgatt  
2401 tatgaacatg gatctcccaa caagagttat ttaaattgat tctcggtctg  
2451 actcgatcgg ttgggttttg agctactcgg tcacaatggg cgggtcgggt  
2501 ctggatctgt tataactaata tttggaagcc tgaagtttca ttgttctgcc  
2551 ccaacttccc actacctttt gaggggtgtta agaagccata caaactaatt  
2601 atgaatccct cccaacaact cagaactcga gtcagtgggt tgtgacgggt  
2651 ctctataaac atttcgaaaa tctttgttca atgaacgtag aaatgaccat  
2701 gcttgatgat tgtgggtctt ataaggtagc tgaccggcgg gcaccggcgg  
2751 ggaggggatt cgctggacca ggctaggtcg aagctggccg gaaaggccag  
2801 ggaggtgaag gacagggcgt cggagttcgc acagcagcat gtcacagggt  
2851 gtcaacagac ctcttaaaga gagtcctcta gttaaattgg tcttcgtttc  
2901 tgtttcgtgg cggcttgtaa actctctttt aagtgtgctg ttttcctttt  
2951 gtctcgtgtg ttgtaagtga aagtgtaatc gaagttccaa gttggagatg  
3001 tttgtaacga tgatgttttc taataatcag agatattaaa agggttgcta  
3051 atttagtatt gcgtctgatc tcggaccaa ctcgcaagta aaattgcaga  
3101 ggatgagttg tacagaacaa gcgtgcattg ttctggaagt tcatctcctt  
3151 ggagccgacc ttgttgcttg cagtttcgcc aagtccacta gacaatgtta  
3201 cgagttaagc ctctgtcaaa cagatcgctc tagcgtccca gaaaacacca  
3251 gatTTTTcga aaaccatcgg ggatcaattt tcgattcaat tccgatcttg  
3301 gaagtacttg aacagaagca tgatgctaaa agataataga aaatcgaagc  
3351 ctagaaaagt tgtacagaaa gcaacaagtc aaaaatatag atcaacttca  
3401 aaggttcaaa ttacatctta cagaccccaa aaaatgacag ttaacagaag

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3451 tcgactaaac agaaaccagc cagcttcacc tggaatgaag gagctttgat  
3501 caatccatcc tagcttcatt cccctttgaa attgcagaca gagctctcat  
3551 cctgctaaag ctggtggctt attcttaacc ctgcaatcaa taagcatgaa  
3601 ctaacattgg acaccttcat cggcggattg ctcgaaaatc agtgagcgag  
3651 ggattttacct gtgtgtgtag taacctctct ccttgtacat aaaatctgga  
3701 aattccggca tcaactactg ccacctttct gcttaagggtg attttatcac  
3751 caaggctgag cgtgattcct tgcgtcttgc tccgaatcct gatgtatcca  
3801 ctgagctttc catctccttc cttctccagg cttatgttca ccaatgcgtc  
3851 ctgcgcgaac acactcttgg cgtacaagtt cgcagccagg aatccacact  
3901 ctccatcaag tgcagacctg caaaccctaa ataagaacac aaactccaaa  
3951 gtcaacgata aattctccgc cttttatgaa gaaaaggaaa cttctgggta  
4001 cttacggtgc cgtcagacac ttcataattg tagacttgat gatatggtcc  
4051 aggaattcct tctcgttctg aattgttgtg ttaacagcaa cctgacagac  
4101 agaaagatat cgcaaattta agatactggg atgactaggc acagagaaat  
4151 gaaatctaata tctagaagta aaaccttatt ttccattca aattctgccc  
4201 acatagtccg gaacgcagca tccgagcaag aagcaggaga gatgtaatcc  
4251 atgatatcga tgtggatatc gttgaggacg acaactgaac gttccatcac  
4301 attgg

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BestFit Results

BESTFIT of: 1587\_SEQ\_1 check: 9861 from: 1 to: 590

to: 6777591\_SEQ\_4 check: 8952 from: 1 to: 3501

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	134	Length:	21
Ratio:	6.381	Gaps:	0
Percent Similarity:	80.952	Percent Identity:	80.952

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 5  
. = 1

1587\_SEQ\_1 x 6777591\_SEQ\_4 December 15, 2006 17:08 ..

```
      .
187 atgtcataaatttttactaaa 207
      ||||| ||| ||| |||
2977 atgtcagaaatccttacgaaa 2997
```

Input Sequence: 1587\_SEQ\_1

!!NA\_SEQUENCE 1.0

1587\_SEQ\_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```
1  gaattcgccc ttggtagatg tctagatgac ctattctact tttcctaaga
51  ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagtttc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatTTtatggT acgggattaa taggttccaa aaaccagccg
301 taacctatTT atattagggt actTTaagct ggtgccctca gTTttgttgg
351 tgtcttcgTT ttTaaactta gTtgtatTTT ttttcttagt tctgtccttc
401 tagtgTTata gagcataagg acaaaattga gcaaaaaatg actaaggata
```

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451 aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatatattag  
501 ttcaaaagga caccagtcta taaaagtat actccaagca catttgaatt  
551 tggatttgca ttgtcagtcg gccagtcga ggggaccatg

Input Sequence: 6777591\_SEQ\_4

!!NA\_SEQUENCE 1.0  
6777591\_SEQ\_4 Length: 3501 December 15, 2006 17:05 Type: N Check: 8952  
..

1 tctagacatt tgacataaac cgaattcaaa gaacacaaca ttgactaaca  
51 ccaaaaagaa atagagtagt gaaatttgga agattaaaaa atagaaacaa  
101 actgattcctt agaaagaaga gatgattagg tgctttcagt tcggtctgtc  
151 aggaaatcga gatgttcact tatttacatt gtcgattcat ctcccaattg  
201 tcctgggttcc ttactgtcc gacgcttttt tgaatcccag ttaattccca  
251 tcaagtcttc cttcagctgc gtagcactgc tagctccaac atggagcgtg  
301 gagtctactc gttcatgggg catcgcaaag gtttgccttc atgttctgct  
351 accagccagc gccaccgcc tcttggttgt gtggacaatt gcggtgaagc  
401 gcgcaagttg acatcccata gtctcgacac ttcaccatat ggatgtttaa  
451 aacgtatatc acgagtgcga tctacatgtc ccatcacacc acatataaag  
501 caatagtttg ggagcttttc atatttgaaa cgggcattga cgacttgccc  
551 tctcgataat ttaatctttt tttctcttca gctgattgtg tgcattccatt  
601 cgggctcaga agcacatcaa agggatctct ccatcgtagt attgggtcgt  
651 gtcgtatgat acgaagcagt cgatgaagtt tcctaattgtg cgagctacag  
701 gtcgcgaaa gaaccgcga ggtagatcgt atgctagtac ccaaaaatca  
751 gtttgtcgta gcggaatcaa cactagagac tcaccctaatt gcatctcatg  
801 tgtgatgaac agtttatcat ttgtgagtct aggggtcatt gtcgatgacc



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851 caatgcacat tgagcttatg atagaatttg aataggaagc gttttccacc  
901 cagatcacga atagctaccc ctttttcggg cgccaaattt ccggcatcct  
951 atcttccacc acaacttaaa gatgcatcg gtaaggaact caccgaccac  
1001 acacatcgaa taatcttcgg tgaccggttc ctgttgatca agtccctcaa  
1051 tttcctcaac ctagtcttca atcgccgcta gcgttatccc ccgcatatgg  
1101 actttcatag cgcgagcgt agccggagac gacgagcaag aaggatgagc  
1151 ggcggcagat tgcggctaaa gaaacgagct tcctgccttg ctctatggag  
1201 gcagatttct gagttgatgg tgatggattt gtgatgtgga cacttttaat  
1251 ttaagttgat tttttagcac ttcattcacg taattaaata aataatttcc  
1301 agtattttat atttatttcc ttacgttatc taattttttg aaagattaaa  
1351 actttgatat aggcaagatc atgacacgtc gaagttaagt gaatgagact  
1401 cctaacaagg taataacaaa gcagttcata aaccgaatga ccttgatcct  
1451 tactaagctt gagatcattg aacatataat taaatacgtt aatgaaagat  
1501 aagaacttta atataaaaaat cattcaaac gagaaactga taacaaaaac  
1551 aaagcaaacg gccaacaaaa taatagacgg tggaaggatg atgcagagcc  
1601 atccaccctt ttttcccagt ttccctactg cttacttctc tatgcatatc  
1651 acaagacgcc cttgaaactt gttagtcatg cagagccctt actcgccagg  
1701 tcaccgcacc acgtgttact ctatcacttc tcctcccttt cctttaaaga  
1751 accaccacgc cacctccctc tcacaaacac tcataaaaaa accacctctt  
1801 gcatttctcc caagttcaaa ttagttcaca gctaagcaag aactcaacaa  
1851 caatggcgga tcgtacaaca cagccacacc aagtccaggt ccacaccag  
1901 caccactatc ccaccggcgg ggctttcggc cgttatgaag gtggactcaa  
1951 aggcggtcca catcaccagc aaggatcagg cagcggccca tcagcttcca  
2001 aggtgttagc agtcatgacc gcgctcccca tcggcgggac cctccttgcc  
2051 ttggccggga taaccttggc tgggacgatg atcgggctgg cgatcaccac  
2101 cccgattttt gtcattctgca gccctgttct agtcccggcc gctctgctca  
2151 tcgggtttgc cgtgagcgcg tttctggcct cggggatggc cgggctgaca

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2201 gggctgacct cgctgtcgtg gtttgcgagg tatctgcagc aggctgggca  
2251 gggagttgga gtgggggtgc cggatagttt cgagcaggcg aagaggcgca  
2301 tgcaggatgc tgctgggtat atggggcaga agaccaagga agttgggcag  
2351 gagatccaga ggaagtctca ggatgtgaaa gcatcagaca aataaggtga  
2401 taataagggg ttttgggttc gtgtgtaaac tggtaaaatg gaaattcttg  
2451 gttttactgt acttttgcac gtagtggaat gaatgagttc ttgttctctt  
2501 ttgtctttta atcataaagt aagaagcagc atttcatgtt ctggttgaat  
2551 attgtcaaga attcgcaaca aatttagcta aaccagttca atcttaccgg  
2601 ttagacgact tcccagtaag aaacattcca ggtccatccc ggtataagag  
2651 tctggacttc tgaaaccttt agaccttgga tttggaaaaa agatgaaacc  
2701 tttagaataa attacaacga tggcagattg tacaaaactg gagtcgagat  
2751 catgtaaatt agcccataac taagaaccgg cgatgacaac aattactagg  
2801 aatatggttg ttgggctggt cggcggttag cggatgatgat ttggaagaat  
2851 cggggatcca gaatgtgaga accgaatcat cgacgaacat taccggcgca  
2901 ggagcccatt tcaagcaact ttggaactcc tatatggctg ttccagcagg  
2951 ccacctgctc aagaaagaaa gaagccatgt cagaaatcct tacgaaatct  
3001 aactggatgc tgatatgaat ccgccagggtg tgcggagttc ttacaggca  
3051 ggatctataa agaagaaaca tgttttgtat tggcattggt gatgttccaa  
3101 gcacgcagcg atctatctcc ggatcctaac aacaaaaata cggattctgt  
3151 aagaaacaag cgcagaaaac ttctgcaacg aaaccactcg tatatttggt  
3201 tctgagttgg agaaagatga ccatactact gtatttggtt gaacttggat  
3251 tggaaccgaa attttgagtt gaaaagcgag tgatcgata taaatttcag  
3301 attcagatta ggatatacta tgagagaagg tagagttacc tgatactaca  
3351 tactgcccat caggggtaaa agttgcctcg atggttgtgt ttggagatgg  
3401 ttccaggcta aatccacaac gctgaacaaa ttaaaagatg aatggatcaa  
3451 tcttcaacct ttacttctgc atttatgagg attggctcaa ggctctctag  
3501 a

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BestFit Results

BESTFIT of: 1587\_SEQ\_1 check: 9861 from: 1 to: 590

to: 6777591\_SEQ\_6 check: 6664 from: 1 to: 1676

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	169	Length:	34
Ratio:	4.971	Gaps:	0
Percent Similarity:	73.529	Percent Identity:	73.529

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 5  
. = 1

1587\_SEQ\_1 x 6777591\_SEQ\_6 December 15, 2006 17:08 ..

```
      .      .      .  
343 tttgttggtgtcttcgtttttaaacttagttgta 376  
    | ||| || |||| ||||| ||| || |  
1617 tatgtatgtttcttggtttttaaattaaatgga 1650
```

Input Sequence: 1587\_SEQ\_1

!!NA\_SEQUENCE 1.0

1587\_SEQ\_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```
1  gaattcgccc ttggtagatg tctagatgac ctattctact tttcctaaga  
51  ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg  
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca  
151 agaaccagcc acaatccatt tattagtttc atataaatgt cataaatttt  
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa  
251 aaacgccagt tatttatggt acgggattaa taggttccaa aaaccagccg  
301 taacctattt atattagggt actttaagct ggtgccctca gttttgttgg  
351 tgtcttcggt tttaaactta gttgtatfff ttttcttagt tctgtccttc  
401 tagtggtata gagcataagg acaaaattga gcaaaaaatg actaaggata
```

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451 aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag  
501 ttcaaaagga caccagtcta taaaagtat actccaagca catttgaatt  
551 tggatttgca ttgtcagtca ggccagtcaa ggggaccatg

Input Sequence: 6777591\_SEQ\_6

!!NA\_SEQUENCE 1.0  
6777591\_SEQ\_6 Length: 1676 December 15, 2006 17:06 Type: N Check: 6664  
..

1 tccactatgt aggtcatatc catcatttta atttttgggc accattcaat  
51 tccatcttgc ctttagggat gtgaatatga acggccaagg taagagaata  
101 aaaataatcc aaattaaagc aagagaggcc aagtaagata atccaaatgt  
151 acacttgtca tcgccgaaat tagtaaaata cgcgccatat tgtattccca  
201 cacattatta aaataaccgta tatgtattgg ctgcatttgc atgaataata  
251 ctacgtgtaa gcccaaaaga acccacgtgt agcccatgca aagttaacac  
301 tcacgacccc attcctcagt ctccactata taaaccacc atccccaatc  
351 ttaccaaaacc caccacacga ctcaaacctc gactctcaca ccttaaagaa  
401 ccaatcacca ccaaaaaatg gcaaagctga tgagcctagc agccgtagca  
451 acgcagttcc tcttctgat cgtggtggac gcatccgtcc gaaccacagt  
501 gattatcgac gaggagacca accaaggccg cgggtggaggc aaggtggcag  
551 ggacagcagc agtctgcgag cagcagatcc agcagcgaga cttcctgagg  
601 agctgccagc agttcatgtg ggagaaagtc cagagggggcg gccacagcca  
651 ctattacaac cagggccgtg gaggaggcga acagagccag tacttcaaac  
701 agctgtttgt gacgacctta agcaattgcg caccgcggtg caccatgcc  
751 ggggacttga agcgtgccat cggccaaatg aggcaggaaa tccagcagca  
801 gggacagcag cagggacagc agcaggaagt tcagaggtgg atccagcaag

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851 ctaaacaaat cgctaaggac ctccccggac agtgccgcac ccagcctagc  
901 caatgccagt tccagggcca gcagcaatct gcatgggtttt gaaggggtga  
951 tcgattatga gatcgtacaa agacactgct aggtgttaag gatggataat  
1001 aataataata atgagatgaa tgtgttttaa gttagtgtaa cagctgtaat  
1051 aaagagagag agagagagag agagagagag agagagagag agagagagag  
1101 agaggctgat gaaatgttat gtatgtttct tggtttttaa aataaatgaa  
1151 agcacatgct cgtgtggttc tatcgaatta ttcggcggtt cctgtgggaa  
1201 aaagtccaga agggcgggcg cagctactac tacaaccaag gccgtggagg  
1251 agggcaacag agccagcact tcgatagctg ctgcatgat cttagcaat  
1301 tgaggagcga gtgcacatgc aggggactgg agcgtgcaat cggccagatg  
1351 aggcaggaca tccagcagca gggacagcag caggaagttg agaggtggtc  
1401 ccatcaatct aaacaagtcg ctagggacct tccgggacag tgcggcacc  
1451 agcctagccg atgccagctc caggggcagc agcagtctgc atggttttga  
1501 agtggtgatc gatgagatcg tataaagaca ctgctaggtg ttaaggatgg  
1551 gataataaga tgtgttttaa gtcattaacc gtaataaaaa gagagagagg  
1601 ctgatggaat gttatgtatg tatgtttctt ggttttttaa attaatgga  
1651 aagcacatgc tcgtgtgggt tctatc

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BestFit Results

BESTFIT of: 1587\_SEQ\_1 check: 9861 from: 1 to: 590

to: 6777591\_SEQ\_8 check: 1234 from: 1 to: 4999

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	445	Length:	379
Ratio:	1.233	Gaps:	7
Percent Similarity:	61.224	Percent Identity:	39.650

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 5  
. = 1

1587\_SEQ\_1 x 6777591\_SEQ\_8 December 15, 2006 17:09 ..

```

      .      .      .      .      .
226 catgtcataactgaacttgtgagaaaaacgccagttatttatggtacggg 275
   ||:  :  :||: | :| ||   |||:|   | | | |:| ||||:|
4543 canaancnangtanatttaaaganatgggaaattaantaatggna.... 4588
      .      .      .      .      .
276 attaatagggttccaaaaaccagccgtaacctatttta.....tattagggg 320
   ||:|:|:| |   :| | | |: |:| | : : |   | |||:|
4589 atnannaggaggattgnaacgggtcnganccgnanganaganagttttanngg 4638
      .      .      .      .      .
321 actttaagctggtgccctcagttttgttggtgtcttcgtttttaaaactta 370
   | | | ||| |   | |:|: | : | :| | | : | |
4639 tttaaatactggg.....gagtngnagccngccnctggttccngtgta 4682
      .      .      .      .      .
371 gttgtatttttttttcttagttctgtccttctagtgttatagagcataagg 420
   | :| |   :| |   | : |:| :::|:| | | | |||
4683 gangaaaccaagnnccggg...aggnttncannngnnaggagagaaaaagg 4729
      .      .      .      .      .
421 acaaaattgagcaa.....aaaatgactaaggataaaaatgaggatat 463
   |:| | |:|:|:|   | ||| : | | : | |:| | |
4730 anncatttnannangcngaggacatgaancggtacngagctgnggttca 4779
      .      .      .      .      .
464 cagaaagggcagcagcttaaaaaaccttt.....tatattagttcaaaa 507
   ::|: | |   |:|: | | :|   : : | | |:|:|
4780 nnnancgg.....cgnnngnagtcnnggggacnnggntggggtnanaa 4824
      .      .      .      .      .
508 ggacaccagtcctataaaaagtatactccaagcacatttgaatttggattt 557
   || |: | |: |:|:|: | |: | : ||| : ||| |||
4825 gggaanggaacattnggtngnangganaaanaccnttttacnattgccttt 4874
      .      .      .      .      .
558 gcattgtcagtcaggccagtcagggggac 586
```

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||| ::: : :|||: |: || :||  
4875 gcaggnngtntnggcncntncgggtnac 4903

Input Sequence: 1587\_SEQ\_1

!!NA\_SEQUENCE 1.0  
1587\_SEQ\_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```
1  gaattcgccc ttggtagatg tctagatgac ctattctact tttcctaaga
51  ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagtttc atataaatgt cataaatTTT
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatTTtatggT acgggattaa taggttccaa aaaccagccg
301 taacctatTT atattagggT actTTaagct ggtgccctca gTTTTgttgg
351 tgtcttcgTT tTTaaactta gttgtatTTT tTTtcttagt tctgtccttc
401 tagtgTTata gagcataagg acaaaattga gcaaaaaatg actaaggata
451 aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcaa ggggaccatg
```

Input Sequence: 6777591\_SEQ\_8

!!NA\_SEQUENCE 1.0  
6777591\_SEQ\_8 Length: 4999 December 15, 2006 17:07 Type: N Check: 1234  
..

```
1  ctcaagcata cggacaaggg taaataacat agtcaccaga acataataaa
51  caaaaagtgc agaagcaaga taaaaaaatt agctatggac attcaggttc
101 atattggaaa catcattatc ctagtcttgt gaccatcctt cctcctgctc
```

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151 tagttgagag gccttgggac taacgagagg tcagttggga tagcagatcc  
201 ttatcctgga ctagcctttc tgggtgtttca gagtcttcgt gccgccgtct  
251 acatctatct ccattaggto tgaagatgac tcttcacacc aacgacgttt  
301 aaggtctcta tcctactcct agcttgcaat acctggcttg caataacctgg  
351 agcatcgtgc acgatgattg gatactgtgg aggaggagtg tttgctgatt  
401 tagagctccc gggtgggtga tttgacttcg atttcagttt aggcttggtg  
451 aaatttttca gggtccattg tgaagccttt agagcttgag ctcccttcca  
501 tgttaatgcc ttgatcgaat tctcctagag aaaaggggaag tcgatctctg  
551 agtattgaaa tcgaagtgca cttttttttt caacgtgtcc aatcaatcca  
601 caaacaagc agaagacagg taatctttca tacttatact gacaagtaat  
651 agtcttaccg tcatgcataa taacgtctcg ttccttcaag aggggttttc  
701 cgacatccat aacgaccga agcctcatga aagcattagg gaagaacttt  
751 tggttcttct tgtcatggcc tttatagggtg tcagccgagc tcgccaatcc  
801 ccgtccgact ggctccgcaa aatattcgaa cggcaagtta tggacttgca  
851 accataactc cacgggtattg agcaggacct attgtgaaga ctcatctcat  
901 ggagcttcag aatgtggttg tcagcaaacc aatgaccgaa atccatcaca  
951 tgacggacgt ccagtgggtg agcgaaacga aacaggaagc gcctatcttt  
1001 cagagtcgtg agctccacac cggattccgg caactacgtg ttgggcaggc  
1051 ttcgccgtat tagagatatg ttgaggcaag acccatctgt gccactcgta  
1101 caattacgag agttgttttt tttgtgattt tcctaagttt ctggttgatg  
1151 gtgagctcat attctacatc gtatgggtctc tcaacgtcgt ttctgtcat  
1201 ctgatatccc gtcatttgca tccacgtgcg ccgcctcccg tgccaagtcc  
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1351 ggggtgacgg tttggtgtgg gttgacggca ttgatcaatt tacttcttgc  
1401 ttcaaattct ttggcagaaa acaattcatt agattagaac tggaaaccag  
1451 agtgatgaga cggattaagt cagattccaa cagagttaca tctcttaaga



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1501 aataatgtaa cccctttaga ctttatatat ttgcaattaa aaaaataatt  
1551 taacttttag actttatata tagttttaat aactaagttt aaccactcta  
1601 ttattttatat cgaaactatt tgtatgtctc ccctctaaat aaacttggtta  
1651 ttgtgttttac agaacctata atcaaataat caatactcaa ctgaagtttg  
1701 tgcagttaat tgaagggatt aacggccaaa atgcactagt attatcaacc  
1751 gaatagattc aactagatg gccatttcca tcaatatcat cgccgttctt  
1801 cttctgtcca catatcccct ctgaaacttg agagacacct gcacttcatt  
1851 gtccttatta cgtgtttacaa aatgaaaccc atgcatccat gcaaactgaa  
1901 gaatggcgca agaacccttc ccctccattt cttatgtggc gaccatccat  
1951 ttcaccatct cccgctataa aacaccccca tcacttcacc tagaacatca  
2001 tcactacttg cttatccatc caaaagatac ccaccatggc tagatcatca  
2051 agccctttgc ttctctcact ctgcattttc gccattctct tccactcttc  
2101 tctgggtagg cagcaattcc agcaggggaa cgagtgccag atcgacagga  
2151 tcgacgcac cagagccggac aaaacccatcc aggcagaagc tggcaccatc  
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2251 tgtaaggcgc accattgagc ccaaaggtct tctcttgcc tttacagca  
2301 acacccctca gctcatctac atcgttcaag gtataaatta aatcagttca  
2351 tacaatgata accaccactt cgaatgtatt tatcaaata caatgatcga  
2401 tgcacctgta tgtgttgtgt atattcaggt aggggagtta caggaatcat  
2451 gttcccakga tgtccagaga cattcgagga atcccagcag caaggacaac  
2501 agggccaaca gggtagttcc caagaccagc accagaagat ccgccgcttc  
2551 cgtgaagggtg acgtcattgc cgtccctgcc ggtgtagccc actggtccta  
2601 caacgatggc aacgaaccag tcatggccat tgttgtccat gacacttcca  
2651 gccacctcaa ccaactggac aacaaccca gggatatata gcattgccgt  
2701 agttgctaata aaattgcaca caattggaac tctattttca gtatctaata  
2751 actttttcct tttttggcag aacttctact tggcaggaaa cccgagagac  
2801 gagttcgaac aatcgagca aggaggcagg ctgagccgtg gggagagtga

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2851 aggtggacga ggacgcaggg aacctcttca acctgcaaca acctcttctt  
2901 gcggaatcga ctccaagctc atcgcgagg cggttcaatgt cgacgagaac  
2951 gtggcaagga ggctacagag cgagaacgac aacagaggcc agatcgtccg  
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3401 gtacgcgata agaggacaag ccagagtcca gatcgtgaac gaggaagga  
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3751 tcaaggaggt gatcaacttg cttatgtaaa atgtgacggt gaaataataa  
3801 cggtaaaata tatgtaataa taataataat aaagccacaa agtgagaatg  
3851 aggggaaggg gaaatgtgta atgagccagt agccggtggt gctaattttg  
3901 tatcgtattg tcaataaatc atgaattttg tggtttttat gtgtttttt  
3951 aaatcatgaa ttttaaat taaaaataa tctccaatcg gaagaacaac  
4001 attccatata catggatgtt tctttacca aatctagttc ttgagaggat  
4051 gaagcatcac cgaacagttc tgcaactatc cctcaaaagc tttaaatga  
4101 acaacaagga acagagcaac gttccaaaga tcccaaacga aacatattat  
4151 ctatactaata actatattat taattactac tgcccgggaat cacaatccct

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4201 gaatgattcc tattaactac aagccttggt ggcgggcgag aagtgatcgg  
4251 cgcgggcgaga agcagcggac tcggagacga ggccttggat gagcagagtc  
4301 tttacctgcc agggcgtaga ggggaagagc ggccttctgg agtaggagtt  
4351 cagcaagcgg cggttccttg gcggagtaag cggacgtaag ggtggntgtc  
4401 gacgtcntcg tttcnggagg cgnattcatg aagggttaaa gtcanatctg  
4451 tagctctcga gtgctcagg agccnaaaga cgttgggaaa ccgtcgnctg  
4501 ttggggcatc agtcngcggg gcacgcttcc ctctgctgc tccanaancn  
4551 angtanattt aaaaganatg ggaaattaan taatggnaat nannaggagg  
4601 attgnaacgg tcnganccgn angaanagtt tttannggtt taaatactgg  
4651 gggagtngna gccngccnct ggttcnctg tagangaaac caagnnccgg  
4701 gaggnntnca nnngnnagg agaaaaagga nncatttnan nangcngagg  
4751 gacatgaanc ggtacngagc tgnggttcan nnancggcgn nnggnagtcc  
4801 cnngggaccn ggntggggtg anaagggaan ggaacattng gtngnangga  
4851 naanaccntt ttacnattgc ctttgcagg nngtntnggc ncntnccgggt  
4901 nacatnccgc tgcattgggt ttggggngcc nanaggnagc cncangggna  
4951 nnngccncc ttgtncangn cgctnaagtt cnattgtana tggncgttg